

GenCore version 5.1.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 : Search time 1441.15 Seconds
(without alignments)
15778.007 Million cell updates/sec

Title: US-09-497-967-5
Perfect score: 1404
Sequence: 1 atgaagaacaacactctggt.....tgatctcttactactgctg 1404

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	54.4	3.9	502	BQ134889	BQ134889 INIT1_1_D
c 2	54.4	3.9	590	BQ135179	BQ135179 INIT1_4_C
c 3	54.4	3.9	602	BQ135164	BQ135164 INIT1_4_B
c 4	54.4	3.9	607	BQ134912	BQ134912 INIT1_1_F
c 5	54.4	3.9	658	BQ135057	BQ135057 INIT1_2_G
c 6	51.2	3.6	445	BQ134871	BQ134871 INIT1_1_B

c 7	50.4	3.6	419	14	BQ135036	BQ135036
c 8	40	2.8	210	14	BQ134900	BQ134900 INIT1_2_D
c 9	40	2.8	538	14	BQ134810	BQ134810 INIT1_1_E
c 10	40	2.8	592	14	BQ134985	BQ134985 INIT1_4_C
c 11	40	2.8	599	14	BQ134821	BQ134821 INIT1_2_G
c 12	40	2.8	661	14	BQ135189	BQ135189 INIT1_4_D
c 13	40	2.8	675	14	BQ135196	BQ135196 INIT1_4_D
c 14	40	2.8	856	9	AL529709	AL529709 AL529709
c 15	39.8	2.8	565	12	BF191747	BF191747 239419 MA
c 16	39.6	2.8	946	17	CNS06Q63	AL410257 T7 end of
c 17	38.4	2.7	938	13	BI950738	BI950738 HVSMEL002
c 18	37.8	2.7	390	13	BI316601	BI316601 saf05d09.
c 19	37.8	2.7	1089	17	CNS06QJ6	AL411124 T7 end of
c 20	37.8	2.7	1089	17	CNS06QJ6	AL410021 T3 end of
c 21	37.6	2.7	479	12	BF776376	BF776376 287167 MA
c 22	37.4	2.7	413	12	BG156079	BG156079 sea0a12.
c 23	37.4	2.7	977	17	CNS02ANA	AL188711 Tetraodon
c 24	37.2	2.6	941	17	CNS056AV	AL323104 Tetraodon
c 25	37	2.6	1177	13	BG915930	BG915930 602815385
c 26	36.8	2.6	877	17	CNS04NWK	AL299261 Tetraodon
c 27	36.6	2.6	328	10	BB497602	BB497602 BB497602
c 28	36.4	2.6	576	9	AL818926	AL818926 AL818926
c 29	36.2	2.6	389	10	AW325085	AW325085 TENUA4390
c 30	36.2	2.6	448	12	BF255972	BF255972 HVSMEL000
c 31	36.2	2.6	473	13	BM098087	BM098087 BBP103_SO
c 32	36.2	2.6	576	12	BG301223	BG301223 HVSMEL001
c 33	36.2	2.6	688	9	AI612588	AI612588 TENG0393
c 34	36.2	2.6	791	9	AJ443260	AJ443260 AJ443260
c 35	36.2	2.6	894	12	BG367203	BG367203 HVSMEL001
c 36	35.8	2.5	256	12	BG301587	BG301587 kt02h09.y
c 37	35.8	2.5	273	13	BM339376	BM339376 MEST240-F
c 38	35.8	2.5	424	9	AI438101	AI438101 sa35h11.y
c 39	35.8	2.5	447	12	BF707190	BF707190 282711 MA
c 40	35.8	2.5	513	10	BE355071	BE355071 DGL_113.G
c 41	35.8	2.5	654	13	BI874624	BI874624 963116H11
c 42	35.8	2.5	669	9	AU169066	AU169066 AU169066
c 43	35.8	2.5	713	17	AZ346186	AZ346186 LM081606
c 44	35.8	2.5	862	12	BG769770	BG769770 602744673
c 45	35.8	2.5	920	12	BG420157	BG420157 602452258

ALIGNMENTS

RESULT 1
BQ134889/c
LOCUS
DEFINITION
BQ134889
502 bp mRNA linear EST 22-APR-2002
multifiliis cDNA, mRNA sequence.
ACCESSION
BQ134889.1 GI:20260988
VERSION
BQ134889.1
KEYWORDS
EST.
SOURCE
Ichthyophthirius multifiliis.
ORGANISM
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 502)
AUTHORS
Clark, I., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
TITLE
An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 474

FEATURES
source

/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site 1: EcoRI; Site 2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 215 a 122 c 122 g 199 t
ORIGIN

Query Match 3.98; Score 54.4; DB 14; Length 658;
Best Local Similarity 51.78; Pred. No. 0.00084;
Matches 155; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

QY 1114 GCTACCTGATCGCTGCTGCTGAGTGTCTGCTGGAACCGTGTGACCGACGGA 1173
DB 315 GCTACTTCAGCCACATATATGTTAAACGATGTCCTGCTGCTGATGATGGT 256
QY 1174 ACCACCTTACCTACACAGCGTCTCTGAGTGTGTGAAGTGTGCTTAACCTTCTAC 1233
DB 255 ACATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTACTTAATGTTAGGCTAACTTTTAT 196
QY 1234 ACCACCAAGCAGCAGCTGGTGGCTGGAATCGACACCTGTACTCTTGTAAACAAG 1293
DB 195 GCATCAAAAACATCTGGTTTGCAGCAGGTACTGATACATGCTGAATGTTCTAAAAA 136
QY 1294 CTGACCTCTGGAGCTGAGCTAACCTGCCTGAGTGTGCTAAGAAGACATCCAGTGTGAC 1353
DB 135 TTAACCTTCTGGTGTACAGCTAAAGTATATGCTGAAGCTACTTAAAGACATAATGCGCC 76
QY 1354 -----TTGCGTAACTTCTGCTATCTCTGCTGCTGCTGCTTCTTACTACCTGCTG 1404
DB 75 AGTTCACCTTTCGCAAAATTTTATCAATGCTTAAATATTTATTTCTTCTATTTGTTG 16

RESULT 6
BQ134871/c
LOCUS
DEFINITION
INIT1_B05.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.

ACCESSION BQ134871
VERSION BQ134871.1 GI:20260970
KEYWORDS EST
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
REFERENCE 1 (bases 1 to 445)
AUTHORS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.

TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.

Seq primer: JEN REV
High quality sequence start: 37
High quality sequence stop: 443
POLYA=Yes.
FEATURES
source Location/Qualifiers
1. .445
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"

/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site 1: EcoRI; Site 2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 155 a 79 c 71 g 140 t
ORIGIN

Query Match 3.68; Score 51.2; DB 14; Length 445;
Best Local Similarity 51.08; Pred. No. 0.005;
Matches 153; Conservative 0; Mismatches 138; Indels 9; Gaps 1;

QY 1114 GCTACCTGATCGCTGCTGCTGAGTGTCTGCTGGAACCGTGTGACCGACGGA 1173
DB 323 GCTACTTCAGCCACATATATGTTAAACGATGTCCTGCTGCTGATGATGGT 264
QY 1174 ACCACCTTACCTACACAGCGTCTCTGAGTGTGTGAAGTGTGCTTAACCTTCTAC 1233
DB 263 TCATCAACTAATTTTGTAGCTTTAGCAAGTGAATGCTCTAAATGTTAGGCTAACTTTTAT 204
QY 1234 ACCACCAAGCAGCAGCTGGTGGCTGGAATCGACACCTGTACTCTTGTAAACAAG 1293
DB 203 GCATCAAAAACATCTGGTTTGCAGCAGGTACTGATACATGCTGAATGTTCTAAAAA 144
QY 1294 CTGACCTCTGGAGCTGAGCTAACCTGCCTGAGTGTGCTAAGAAGACATCCAGTGTGAC 1353
DB 143 TTAACCTTCTGGTGTACAGCTAAAGTATATGCTGAAGCTACTTAAAGACATAATGCGCC 84
QY 1354 -----TTGCGTAACTTCTGCTATCTCTGCTGCTGCTGCTTCTTACTACCTGCTG 1404
DB 83 AGTTCACCTTTCGCAAAATTTTATCAATGCTTAAATATTTATTTCTTCTATTTGCGC 24

RESULT 7
BQ135036/c
LOCUS
DEFINITION
INIT1_D10.gl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.

ACCESSION BQ135036
VERSION BQ135036.1 GI:20261135
KEYWORDS EST
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis.
REFERENCE 1 (bases 1 to 419)
AUTHORS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.

TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.

Seq primer: T7
High quality sequence start: 306
High quality sequence stop: 419
POLYA=Yes.
FEATURES
source Location/Qualifiers
1. .419
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"

KEYWORDS
EST.
SOURCE
ORGANISM
Ichthyophthirius multifiliis.

REFERENCE
AUTHORS
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.

TITLE
JOURNAL
COMMENT
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 506
POLYA=No.

FEATURES
source Location/Qualifiers
1..599
 /organism="Ichthyophthirius multifiliis"
 /strain="G5"
 /db_xref="taxon:5932"
 /clone_lib="G5 trophont cDNA (INIT1)"
 /note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 191 a 113 c 111 g 183 t 1 others
ORIGIN

Query Match 2.8%; Score 40; DB 14; Length 599;
Best Local Similarity 58.3%; Pred. No. 6.5;
Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1114 GCTACCGTGATGGTCAGTGTGCTCTGGAGTGTCTCTGCAACGGTGCTCACCGCGGA 1173
|||| | ||| | |||| | ||||| ||||| ||| | ||||| ||| | ||||| ||| | ||||| |||
Db 349 GCTAAATTAGCGCATATAATGGCACTGAATGTCTGTGGCAGCTCTTTGTACAGACGGA 290
|||| | |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1174 ACCACCTTACTACAACGAGCGTCTTCTGAGTGTGTGAAGTGTGTCTTAACCTTCTTAC 1233
|| |||| | ||| | |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 289 GTAACACCTACTATTACTGTATCATCTCTCAATGTTGTTAATTGTAAGGTGGCTTTTAC 230

RESULT 12

BQ135189 661 bp mRNA linear EST 22-APR-2002
LOCUS
DEFINITION
INIT1.4_D09.gI_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.

ACCESSION
VERSION
BQ135189
BQ135189.1 GI:20261288

KEYWORDS
SOURCE
EST.
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis

REFERENCE
AUTHORS
Eukaryota; Alveolata; Gliophora; Oligohymenophorea;
Hymenostomatida; Oporyoglenina; Ichthyophthirius.
1 (bases 1 to 661)
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.

TITLE
JOURNAL
COMMENT
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

[illegible]